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Index selection can improve the selection efficiency in a rice recurrent selection population

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Abstract To attain success with selection process, the breeders need to understand the genetic variability into each population developed by breeding program. In this purpose, breeders need to estimate the variance components and genetic and phenotypic parameters. Besides, they need to have the ability to select simultaneously genetically top progenies for multiple traits. This study used a field trial, with a panel of 198 $S_{0:2}$ lowland rice progenies, evaluated in three environments during two years in order to: (*i*) estimate genetic parameters for different traits in a rice breeding population, (*ii*) evaluate the impact of direct selection and selection performed through three selection indices in a rice population developed by recurrent selection, and (*iii*) compare three selection indices using different economic weights with direct and indirect selection. Significant genetic variation was found among progenies for: grain yield, plant height, days to flowering, panicle blast, leaf scald and grain discoloration. The direct selection provided high gains for single trait selection, but this method may results in undesirable changes in related traits. Thus, between the evaluated indices and in comparison, to indirect selection the Mulamba and Mock index provided simultaneously greater gains for all the evaluated traits. Furthermore, we found that when the random weights and *b*-variation index were used as economic weight, it was found lower gains or no gains, showing that the gains attained with Smith and Hazel and Tai indices were linked to economic weights used.

Keywords Genetic improvement · Quantitative genetics · Predicted gains · Economic weight

Abbreviations

DAS	Days after the sowing
GY	Grain yield
PH	Plant height
DF	Days to flowering
PB	Panicle blast
Ls	Leaf scald
Gd	Grain discoloration
ANOVA	Analysis of variance
σ_g^2	Genetic variance
σ_P^2	Phenotypic variance
σ_e^2	Error variance among plots
h^2	Broad-sense heritability
CV_g	Genotypic coefficient of variation

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R^2	Coefficient of determination
DS	Direct selection
IS	Indirect selection
SH	Smith and Hazel index
TA	Tai index
MM	Mulamba and Mock index
GSD	Genetic standard deviation
RW	Random weights
MANOVA	Multivariate analysis of variance
G x E	Genotype x environment interaction

Introduction

A main goals of rice breeding programs is to develop cultivars with high yield potential (Khan et al. 2015) and high grain quality (Asante 2017). However, it has been well recognized that these traits, such as, others important economically traits, as plant height (Wang et al. 2016; Ansari et al. 2017) and resistance to diseases (Hashioka 1950; Dai et al. 2007; Sato et al. 2008; Ballini et al. 2008) have quantitative inheritance. Thus, in a breeding program is important manipulate efficiently multiple genes, which makes the breeding process more laborious. One efficient strategy to manipulate multiple genes is the recurrent selection. This refers a cyclical selection method performed of repetitive manner to gradually increase the frequency of favorable alleles in a population, allowing the maintenance of genetic variability and increasing the probability to select the best lines with continuous gains by selection (Jenkins 1940; Bernardo 2002; Hallauer et al. 2010). In rice, some advances for grain yield have been achieved using the recurrent selection, with gains varying from 1.44% (Breseghello et al. 2011), 1.54% (Morais Júnior et al. 2015; Barros et al. 2018) and 3.6% (Breseghello et al. 2009) for upland rice and 1.56% (Rangel et al. 2002) to 1.59% (Streck et al. 2018) for irrigated rice.

Due to rice importance as main daily carbohydrate source for more than half of the world's population for their livelihood, the breeding programs aim to develop more productive and adapted cultivars to supply the market demand (Fairhust and Dobermann 2002; Souza et al. 2007; Qian et al. 2016). Therefore, rice breeders have been focused on improvement of some traits as: grain yield, grain quality, plant height, days to flowering and resistance to diseases (Oladosu et al. 2018; Zarbafi et al. 2019; Lakshmi et al. 2020). Some of these traits are positively (i.e. plant height) or negatively correlated (i.e. flowering date) with grain yield (Kole et al. 2008; Devi et al. 2017; Kumar et al. 2018). In this way, the breeders need to understand the degree of association, the magnitude and nature of the variation of each target trait, on the improvement of each one, once the improvement of one trait can results in a significant losses in others (Zahid et al. 2006; Fotokian and Agahi 2014; Osundare et al. 2017). Thus, the selection performed for one or few traits may result in superior genotypes for only one or few traits (Bárbaro et al. 2007; Pedrozo et al. 2009; Vasconcelos et al. 2010).

An alternative to increase the effectiveness of selection process is performing the selection combining multiple traits through selection indices (Entringer et al. 2016; Coutinho et al. 2019). This method allows to get simultaneous gains even for the traits with adverse effects, as genetic linkage or pleiotropy (Santos et al. 2007). Different selection indices have been proposed by: Smith (1936) and Hazel (1943), Willians (1962), Elston (1963), Pesek and Baker (1969), Cunningham et al. (1970), Subandi et al. (1973), Tai (1977), Mulamba and Mock (1978), Mendes et al. (2009) and Silva et al. (2016a). These methods allow to combine the information of different traits measured in each trial, establishing an optimal linear combination between them, which can increase the selection efficiency (Hallauer et al. 2010; Cruz et al. 2012). Despite this, these indices have not yet been used in the breeding programs routine, the main reason is the difficulty to assign meaningful economic weights for each trait (Marinho et al. 2014; Vieira et al. 2016; Vittorazzi et al. 2017). An alternative to overcome this bottleneck could be the replacement of economic weights by the desired gains as suggested by Pesek and Baker (1969) or to assign the equivalent of one genetic standard deviation for each measured trait (Crosbie et al. 1980).

Several studies for different food crops have been successfully analyzed the selection indices such as in: rice (Rabiei et al. 2004; Smirdele et al. 2019; Venmuhil et al. 2020), bean (Mendes et al. 2009; Marinho et al. 2014), sugarcane (Pedrozo et al. 2009; Almeida et al. 2014), soybean (Gesteira et al. 2018; Freiria et al. 2019) and maize (Crevelari et al. 2017; 2018). Despite these promising results, the use of

selection indices in rice breeding is not yet greatly reported. In order to select promising progenies based on the morpho-agronomic traits, the objectives of this study were to: (*i*) estimate genetic parameters for different traits in a rice breeding population, (*ii*) evaluate the impact of direct selection and selection performed through three selection indices in a rice population developed by recurrent selection, and (*iii*) compare three selection indices using different economic weights with direct and indirect selection.

Material and methods

Genetic material

The genetic material consisted of 198 progenies $S_{0:2}$ of second cycle of CNA 12 population of lowland rice and four commercial rice cultivars. This population was synthesized in 2002 by the rice breeding program at the Brazilian Agricultural Research Corporation (Embrapa Rice and Beans), as a genetically broad-based population with stable genetic resistance to *Magnaporthe oryzae* (anamorph *Pyricularia grisea* Sacc.). More details about CNA 12 population synthesis can be found in Rangel et al. (2003) and Morais Júnior et al. (2017a).

Experimental conditions

The trials were performed in three experimental stations during two seasons (summer season). The experimental stations were located in Goianira, GO, Brazil (16°26′14"S, 49°23′50"W at 720 m above sea level), Formoso do Araguaia, TO, Brazil (11°50′8.01"S, 49°39′19.81"W at 240 m above sea level) and Cantá, RR, Brazil (2°48′29"N, 60°39′19" W at 61 m above sea level). In the first year, the progenies were evaluated in Goianira and Formoso do Araguaia, and in the second year, the progenies were evaluated in Cantá and Goianira.

The trials were carried out in a lowland area with continuous flooding until grain maturity, following a Federer's augmented block design. Except for the trial carried out in Goianira in the second year, which was carried out with two replicates for each progeny, the trials performed in Goianira (first year), Formoso do Araguaia and Cantá were carried out without replicates for progenies. Each trial was performed using 11 blocks with 22 plots per block. Plots consisted of four rows of five meters, with row space of 0.25 m, and 60 seeds per meter, manually sown. The fertilization consisted of applying 500 kg ha^{-1} of 04-28-20 (NPK) + Zn. Topdressing fertilization was performed using 150 kg ha^{-1} of urea in two times: first at 15 days after the sowing (DAS) and the other at 45 DAS using 75 kg ha^{-1} N in each one. The technical itinerary for the crop management was performed similarly to those in commercial production, except to fungicide application. In our case, the fungal diseases were not chemically controlled, once, disease tolerance was part of the experimental assessment. When as needed, weeds and insect pests were controlled via mechanized spraying.

The agronomic traits mesuared at each environment were: grain yield (GY, kg ha^{-1}): measured in the useful area being the two central rows (2 m^2) through harvesting of all grains in each plot, which were dried to 13% of humidity; plant height (PH, cm): taken from the ground to the tip of the main tiller; days to flowering (DF, days): number of days from sowing to 50% of plants at anthesis; panicle blast (PB, scale), leaf scald (Ls, scale) and grain discoloration (Gd, scale): the evaluation was visual, taking account the percentage of panicles, leaf area and grains affected for blast, scald and spot. The grades were assigned according to visual diagrammatic scale which varied from 0 (no incidence) to 9 (more than 50% of infected leaves and/or panicles) (IRRI 2002).

Statistical data analysis

The experimental design was Federer's augmented block, with genotypes (progenies and commercial rice cultivars) and environment as factors. Firstly, the analysis of variance (ANOVA) was performed by environment to evaluate whether or not the ANOVA assumptions were met. After these preliminary evaluations, a joint variance analysis was performed for all the traits. Prioritizing to preserve the interaction between genotype x environment (Goianira, Cantá and Formoso do Araguaia), in the joint analysis, the effects of year and replicates at Goianira were mistaken with block effect, through their convenient re-identification, fitting the following linear model:

$$Y_{iklm} = \mu + l_l + b_{k/l} + t_m + g_{i/m} + tl_{ml} + gl_{il/m} + e_{iklm}$$

where,
Y_{iklm}: is the observed value of ith genotype, in the lth environment in kth block, belonging to type m.

μ: the constant inherent to all observations.

l_l: is the fixed effect of lth environment, l (l = 1, 2, …,L).

$b_{k/l:}$ is fixed effect of kth block, k(k= 1, 2, …, K), within lth environment (k varing from 1 to 11 in Goianira in the first year; from 12 to 22 in Cantá, Formoso do Araguaia and Goianira (first replicate in the second year) and from 23 to 33 in Goianira (second replicate in the second year).

t_m: is the fixed effect of type m (m= 2, with a group of progenies and another of controls).

$g_{i/m}$: is the effect of ith genotype (progenies of random effect and controls of fixed effect) within type m (i= 1, 2,…, P, $P+1$, $P+2$, …, $P+C$, where P is the number of progenies and C is the number of controls), considering $g_{i/m} NID \cap \left(0, \sigma_g^2\right)$.

tl_{ml} : is the fixed effect of the interaction between type m and lth environment.

gl_{il}: is the random effect of the interaction between ith genotype and lth environment, considering $gl_{il} NID \cap \left(0, \sigma_{gl}^2\right)$.

e_{iklm} : is the average experimental error associated with the $iklm$th plot, considered as independent and identically distributed, under $NID \cap (0, \sigma^2)$.

Based on the mathematical expectation of the mean squares, the following variance components and genetic and phenotypic parameters were estimated using the expressions described by Vencovsky and Barriga (1992) and Vencovsky (1987): error variance among plots (σ_e^2), genetic variance (σ_g^2), phenotypic variance (σ_P^2), broad-sense heritability (h^2), genotypic coefficient of variation (CV_g) and b-variation index. The coefficient of determination (R^2) was estimated for the attainment of the contribution of each source of variation to the total variance, as following (Ramalho et al. 1998):

$$R_i^2 = \frac{SS_{qi}}{SS_{qT}}$$

where,
SSq_i: is the sum of squares for ith source of variation.

SSq_T: is the total sum of squares.

Selection strategies

For the selection of top progenies GY and PH were considered as main traits. The following methodologies were used for estimation of expected gains: direct selection (*DS*), indirect selection (*IS*) (performed in grain yield) and three selection indices: *SH*—Smith (1936) and Hazel (1943), *TA*—Tai index (1977) and *MM*—sum of ranks (Mulamba and Mock 1978). For the first two indices were assigned the following economic weights: (*i*) genetic standard deviation (*GSD*), corresponding 1 standard deviation for GY and zero for the others traits; (*ii*) *b*-variation index and (*iii*) random weights (*RW*): the weights −1, 0, 1, 1, 1, 1, were assigned for the traits GY, PH, DF, PB, Ls and Gd, respectively. These weights are the same used by Rodríguez et al. (1998). One the main bottlenecks in the use of selection indices, is the estimation of economic weights (Rodríguez et al. 1998; Ramalho et al. 2012). Despite, it is possible to assign economic weights to *MM* index, here no weights were assigned to *MM* index, which represents an advantage for this index over other indices as Smith and Hazel and Pesek and Baker indices (Crosbie et al. 1980; Cruz and Carneiro 2006).

The classic index proposed by Smith (1936) and Hazel (1943) is a linear combination of multiple traits with economic importance, in which the weighting coefficients are estimated to maximize its correlation with the genotypic aggregate. The genotypic aggregate consisted of a linear combination, including the genetic values of traits, which were weighted by its respective economic weights (Cruz and Carneiro 2006). The classic index was established by the following expression:

$$\widehat{b} = P^{-1}Ga$$

where,
$\widehat{b}$: is the vector of index coefficients.P^{-1} : is the inverse of phenotypic variance-covariance matrix between the traits.

G: is the genetic covariance matrix.

a: is the vector of relative economic weights.

Tai index (Tai 1977) is a generalization of the desired gains index proposed by Pesek and Baker (1969). The Tai index allows the inclusion of secondary traits to aid in the improvement of main traits, the estimation of this index involves the knowledge of expression for the expected gains for each trait, as following:

$$\hat{b} = G^{-1}\Delta g_d$$

where,
G^{-1}: is the inverse of the genotypic variance-covariance matrix between traits.

Δg_d: is the vector of desired gains.

The index of Mulamba and Mock (1978), consist in ranking the genotypes for each trait in favorable order to breeding. The ranking of each genotype for each trait are added, resulting in the following selection index: $I = r_1 + r_2 + \ldots + r_{jn}$, where, I: is the index of ith progeny; r_{jn}: is the rank of ith progeny for jth trait.

The multivariate analysis of variance (MANOVA) was performed to obtain the G matrix (variances and covariances) among the measured traits, using the data from all the genotypes, traits, and environments. The multivariate analysis was performed using the PROC MANOVA statement, which provided the sum of squares matrices and the product for the genotype i, the error e and its degrees of freedom. The statistical analysis was carried out with SAS software version 9.4 (Statistical Analysis System—SAS Institute 2013). All the matrix operations for prediction of selection indices and genetic and phenotypic parameters were performed using BrOffice.org Calc application (www.broffice.org). The *ggplot2* package was used to construct box-plots to visualize the variability of selected population in each selection strategy (Wickham 2009). Other figures were performed using the same package using R Statistical Software (R Core Team 2020).

Genetic gain from direct and indirect selection

The expected gains were estimated among progenies based on three selection criteria: direct selection, indirect selection and selection indices (*SH*, *TA* and *MM*) considering the selection of 25% of top progenies. The expected gains from direct selection for each trait were estimated according to the equation described by Vencovsky and Barriga (1992):

$$SG_{ii}(\%) = \left(\frac{\left[\overline{X}_{si} - \overline{X}_{oi}\right] x h_i^2}{\overline{X}_{oi}}\right) \times 100$$

where,
SG_{ii}: is the gain with direct selection carried for ith trait;

$\bar{X}_{si}$: is the mean of ith trait for the selected progenies.

$\bar{X}_{oi}$: is the mean of ith trait in the base population.

h_i^2: is the heritability for ith trait.

The gains from indirect response to selection were estimated using the following expression described by Vencovsky and Barriga (1992):

$$SG_{j(i)}(\%) = \left(\frac{\left[\overline{X}_{sj} - \overline{X}_{oj}\right] x h_j^2}{\overline{X}_{oi}}\right) \times 100$$

where,
$SG_{j(i)}$: is the gain on jth trait, with selection based in ith trait.

$\bar{X}_{sj}$: is the mean of jth trait for the selected progenies based on ith trait.

$\bar{X}_{oj}$: is the mean of jth trait.

h_j^2: is the heritability of jth trait.

Results

Genetic variability and genetic parameters

A summary of phenotypic traits and two-way ANOVA for all the traits is provided in the Fig. 1. The progenies displayed large variations for the evaluated traits

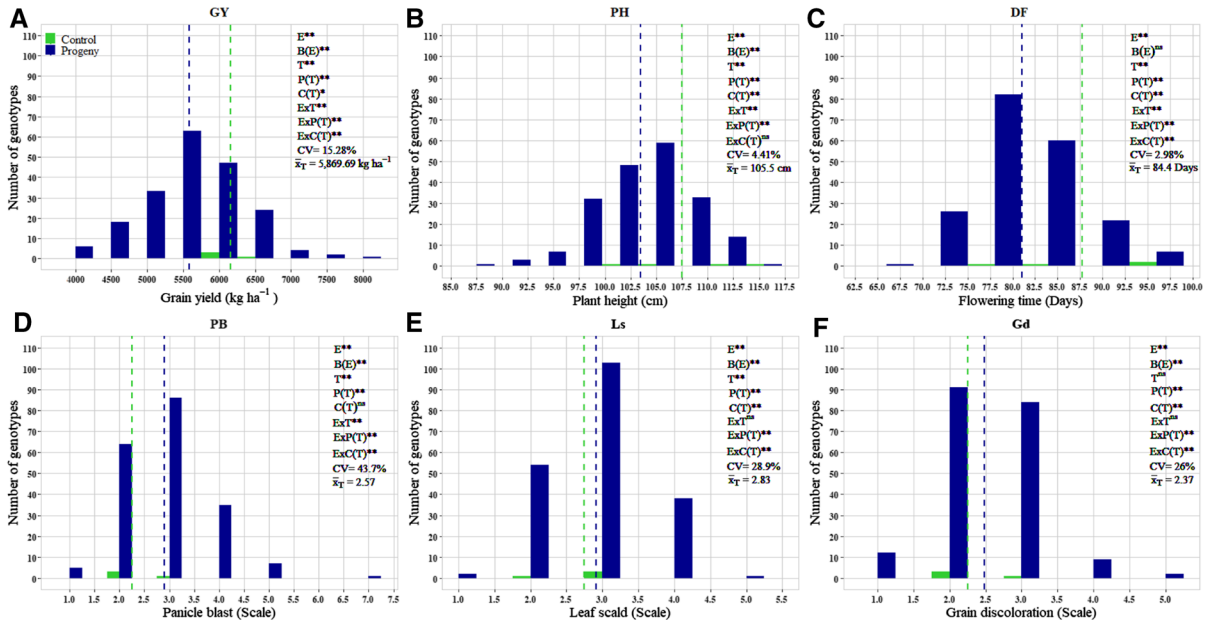

Fig. 1 Frequency distribution of the evaluated traits in $S_{0:2}$ progenies from CNA 12 population. *GY: grain yield, PH: plant height, DF: days to flowering, PB: panicle blast, Ls: leaf scald and Gd: grain discoloration. ns Non-significant; * and ** significant by the t-test at 5 and 1% probability, respectively; E: environment; B(E): block within environment; T: type; P(T): progeny within type; C(T): control within type; ExP(T): interaction between environment and progenies within type; ExC(T): interaction between environment and controls within type; CV: coefficient of variation.* $\bar{x}_T$*: is the overall average (progenies + controls). Dashed lines represent the progenies average (blue dash) and controls average (green dash)*

across the different environments. As commonly found in rice diseases studies, the coefficients of variation (CVs) displayed high values, ranging from 26% to 43.7% (Fig. 1d–f), since they cumulated variations due to the system of evaluation (no metric scale), genetic variability and inter-environments variability, which may have contributed to the high CVs. As expected, the days to flowering (DF), plant height (PH), grain yield (GY), panicle blast (PB), leaf scald (Ls) and grain discoloration (Gd) displayed high variability, mainly for the first three traits, with its CVs varying from 2.98% to 4.41% and 15.28% respectively (Fig. 1a–c).

Partitioning the overall population mean into progenies and controls averages, we found that progenies average was lower than controls average (Fig. 1). Despite this result, it should be highlighting that the evaluated progenies are in the second cycle. In this way, the amplitudes of means among $S_{0:2}$ progenies showed the potential of the CNA 12 population to generate superior inbreds. Except for Gd (Fig. 1f) all evaluated traits had significant type effect, indicating differences in progenies behavior in relation to the controls. The significant mean sum of squares of progenies provides evidence that the progenies were diverse with large genetic variability that can be exploited in rice breeding program through selection. Likewise, the joint analysis showed highly significant difference for progeny x environment interaction ($P< 0.01$), indicating that progenies response varied across the environments (Fig. 1). The presence of genotype x environment interaction is frequently reported in rice studies (Liang et al. 2015; Balakrishnan et al. 2016; Jadhav et al. 2019).

Except to PH (18.4%) and PB (21.2%) (Fig. 2b and d), the largest variation in the main effects was due to environment effect, accounting for 32.5% (GY), 40% (Gd), 49.7% (Ls) and 60.5% (DF) of the sum of squares, being more than two (Gd) (Fig. 2f) and three (GY, DF and Ls) times, the variance explained by the progeny effect (Fig. 2a, c and e). The relatively high contribution of the environment for the total variation was not unexpected, once, we found significant environment effect ($P< 0.01$) for all the traits (Fig. 1). Moreover, the three environments spanned a broad range of rice crop environments, including

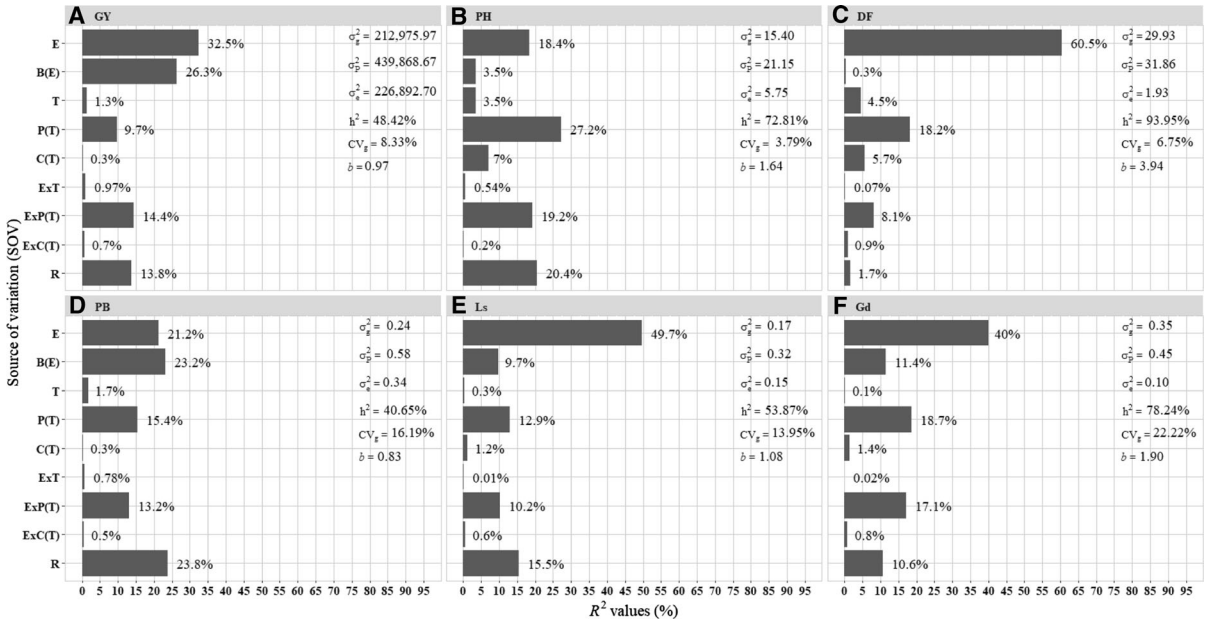

Fig. 2 Estimates of coefficient of determination (R^2) for the sources of variation (*SOV*), components of variance and genetic parameters of $S_{0:2}$ progenies from CNA 12 population. *GY: grain yield, PH: plant height, DF: days to flowering, PB: panicle blast, Ls: leaf scald and Gd: grain discoloration. E: environment; B(E): block within environment; T: type; P(T): progeny within type; C(T): control within type; ExP(T): interaction between environment and progenies within type; ExC(T): interaction between environment and controls within type and R: residuals.* σ_g^2*: genetic variance;* σ_P^2*: phenotypic variance;* σ_e^2*: error variance;* h^2*: broad-sense heritability;* CV_g*: genotypic coefficient of variation and b-variation index*

tropical and equatorial climates and distinctive dry and wet seasons (IBGE 2002). Furthermore, the environment effect was mistaken with year effect, making impossible, with such data set, to isolate them to evaluate the importance of each one in the total variation. By contrast, for all the traits the environment x progenies/type variance (ranging from 8.1% to 19.2%) was more pronounced than environment x control /type (ranging from 0.2% to 0.9%) (Fig. 2). This finding is linked to the inbreeding degree for the evaluated progenies, since within progenies $S_{0:2}$ (equivalent to the $F_{2:4}$ generation for the allelic frequency of 0.5), the genetic variance (considering only additive and dominance effects) is equivalent to 3/4 of the additive variance and 3/8 of the dominance variance, whereas, within inbreds (controls), the genetic variance is equal to zero (Cockerham 1963).

The summary of the estimated variance components and genetic and phenotypic parameters are given in Fig. 2. Except to GY and PB, it was found that in the phenotypic variance, the contribution of genetic effects outweighs the environmental effects for all traits ($\sigma_g^2 > \sigma_e^2$) (Fig. 2a and d). Even so, the estimated broad-sense heritability (h^2) varied greatly between evaluated traits, ranging from 48.42 (GY) to 93.95% (DF), given these traits are quantitative and highly influenced by the environment (Rao et al. 2017; Li et al. 2018; Kumar et al. 2019; Zhang et al. 2020). The highest values to h^2 were found for DF (93.95%), followed by Gd (78.24%) and PH (72.81%) (Fig. 2c, f and b), indicating that these traits are highly heritable among the evaluated progenies, increasing the probability of gains with selection for each one. These results can be confirmed by the values found for *b*-variation index that were greater than 1, 3.94 (DF), 1.90 (Gd) and 1.64 (PH) (Fig. 2c, f and b), which can results in a greater genetic variability, suggesting favorable conditions for selection (Vencovsky 1987; Silva et al. 2008a; Cruz et al. 2012). By contrast, moderate estimates of h^2 were found for Ls (53.87%), GY (48.42%) and PB (40.65%) (Fig. 2e, a, and d). Coincidentally, GY and PB showed *b*-variation index values lower than unit, 0.97 and 0.83 respectively (Fig. 2a and d), and for Ls this value was close to 1 (*b*-variation = 1.08) (Fig. 2e). This finding can be due to

the dominant effect of the environment on crop (Fellahi et al. 2018).

The estimates of genotypic coefficient of variation (CV_g) ranged from 3.79% to 22.22% (Fig. 2). The highest CV_g was observed for Gd (22.22%) followed by PB (16.19%) and Ls (13.95%) (Fig. 2f, d and e). By contrast, low CV_g values were found for PH (3.79%) and DF (6.75%) (Fig. 2b–c). Despite the low variability described by CV_g for these traits, the progenies average for PH and DF were lower than control average (Fig. 1b–c). Here it is necessary to highlight which the value found for CV_g to GY was below 10%, which can difficult the breeder understanding about the genetic variability and advances through selection for grain yield (Oliveira et al. 2015).

Expected genetic gains for the different used selection methods

The selection gains (*SG*%) for direct and indirect selection considering the selection of 25% of top progenies for each trait are shown in Fig. 3. The gains estimates varied widely between the different selection methods. As expected, the gains with direct selection (*DS*) (Fig. 3a) were higher than those found with indirect selection (*IS*) (Fig. 3b), showing high values for Gd (-24.6%) followed by Ls (-15.66%) and PB (-12.83%). Likewise, it was found genetic gains for DF (-7.5%), PH (-4.3%) and GY (7.12%) (Fig. 3a). The positive *SG*% values ensured for GY and the negative values for PH, DF, PB, Ls and Gd is desirable, once, in the breeding programs it seeks for

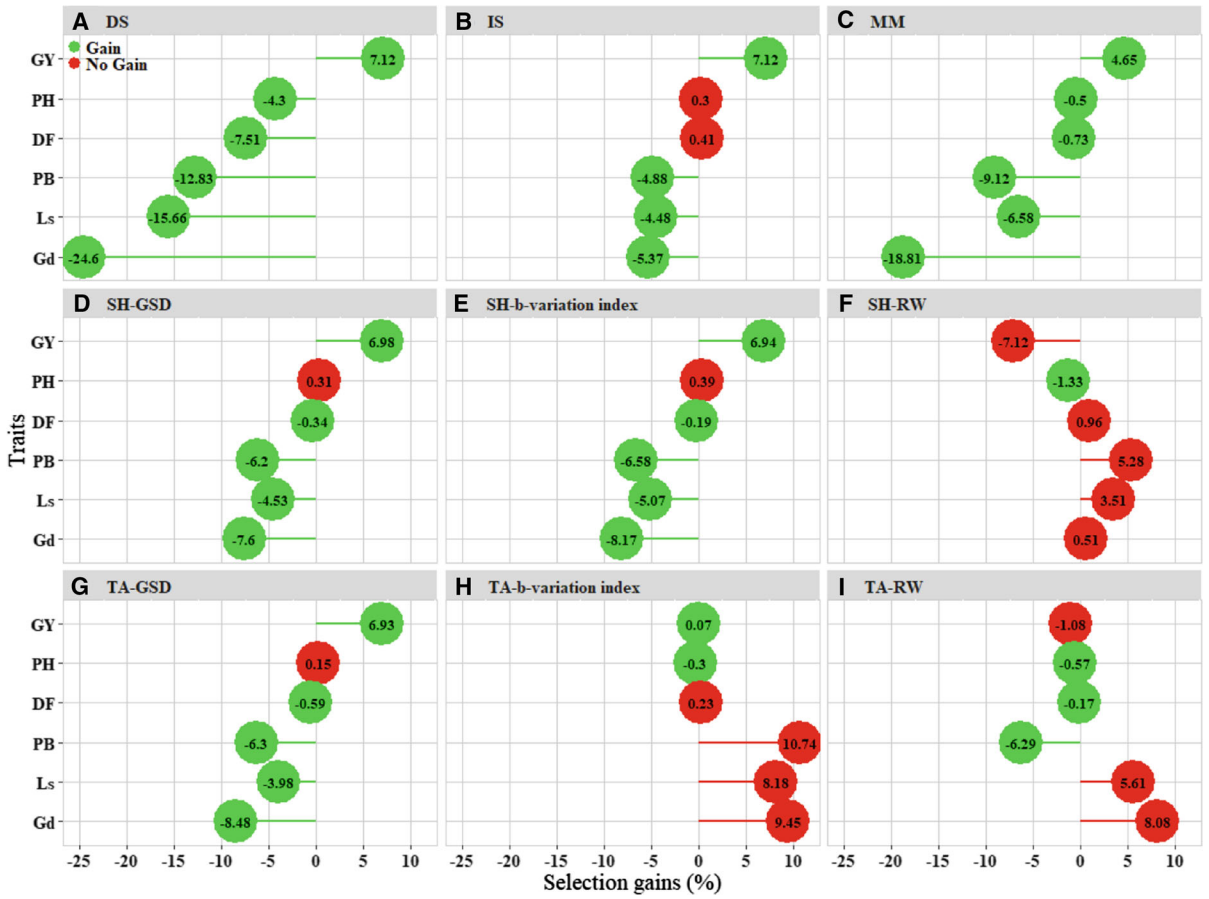

Fig. 3 Selection gains (*SG*%) in $S_{0:2}$ progenies of the CNA 12 population using four different methods. *Direct* (*DS*) *and indirect selection* (*IS*), *Smith and Hazel* (*SH*), *Tai* (*TA*) *and Mulamba and Mock* (*MM*) *selection indices based on three economic weights* (*GSD - genotypic standard deviation, b-variation index and RW - random weights). GY: grain yield, PH: plant height, DF: days to flowering, PB: panicle blast, Ls: leaf scald and Gd: grain discoloration*

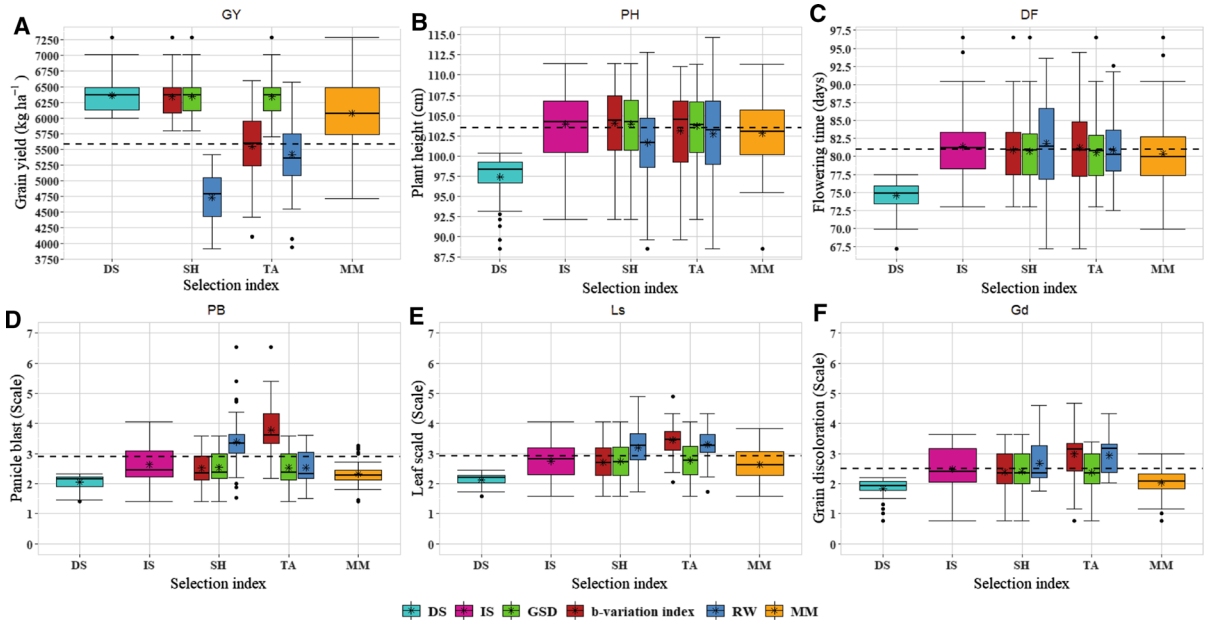

Fig. 4 Average variation of the progenies selected by different selection methods in $S_{0:2}$ progenies from CNA 12 population. *DS*: *direct selection, IS*: *indirect selection, SH*: *Smith and Hazel, TA*: *Tai and MM*: *Mulamba and Mock. Selection indices based on three economic weights* (*GSD - genotypic standard deviation, b-variation index and RW—random weights). GY: grain yield, PH: plant height, DF: days to flowering, PB: panicle blast, Ls: leaf scald and Gd: grain discoloration. Dashed line represents the population average and * the average of the selected progenies*

genotypes with high grain yield, earlier plants, reduced plant height and lower incidence of diseases.

Despite the gains with *DS* were higher than those found with *IS*, the exclusive use of *DS* can be limiting in a breeding program, once here, the selection performed in GY provided positive gains for PH (0.3%) and DF (0.41%) (Fig. 3b–c), indicating, when the selection was performed in GY, plant height and plant cycle were increased in the CNA 12 population (Fig. 4b–c). Through these results, it becomes evident the complexity of simultaneous selection for multiple traits. Thus, the use of selection indices turns an interesting and easier strategy, once its results displayed wide variability between the three indices analyzed (Fig. 3c–i). The gains based in selection index ranged from -18.81% (*MM*) (Fig. 3c) to 6.98% (*SH*) (Fig. 3d). Not surprisingly, independently of the selection index used, the different economic weights assigned provided differences in the predicted gains (Fig. 3d–i).

Between the three evaluated indices, *MM* index provided the best gains for Gd (−18.81%) PB (−9.12%) and Ls (−6.58%) (Fig. 3c). Likewise, this index displayed gains for GY (4.65%), DF (−0.73%) and PH (−0.5%). *MM* index, provided lower gain for GY in comparison to the gains found with *IS*, *SH* and *TA* indices for the same trait (Fig. 3b and d–i). However, with *MM* index was possible to improve the main traits (GY and PH) and the secondary traits (DF, PB, Ls and Gd) simultaneously. The selection based in this index showed an increase in GY mean in relation to population average. Besides, the averages for PH, DF, PB, Ls and Gd for the selected progenies were lower than population average (Fig. 4b–f), indicating that the selection based on *MM* index may be superior as compared to indirect single trait selection.

The selection-based in the *SH* index associated to *GSD* showed gains for Gd (−7.6%), GY (6.98%), PB (−6.2%), Ls (−4.53%) and DF (−0.34%). In same sense, the selection performed with *SH-b*-variation index displayed desirable gains in Gd (−8.17%), GY (6.94%), PB (−6.58%), Ls (–5.07) and DF (–0.19%) (Fig. 3d). Despite *SH* index, not provided gains for PH, the gains presented with this index associated to *GSD* and *b*-variation index (Figs. 3d–e), were higher than those found when the selection was performed in GY (*IS*) (Fig. 3b). By contrast, when *RW* were

assigned to *SH* index as economic weight, except for PH (−1.33%), no gains were found for GY (−7.12%), DF (0.96%), PB (5.28%), Ls (3.51%) and Gd (0.51%) (Fig. 3f).

Coincidentally, the prediction of desired gains based in *TA* index associated to *GSD* (Fig. 3g), showed gains close to the gains found with *SH-GSD*, *SH-b*-variation index and *IS* (Fig. 3d–e and b). The selection performed with *TA-GSD*, showed high gains for Gd (−8.48%), GY (6.93%), PB (6.3%) and Ls (−3.98%) and lower gain for DF (−0.59%) (Fig. 3g). The *b*-variation index assigned as economic to *TA* index showed low gains for GY (0.07%) and PH (−0.3%) and no gains were observed for the others traits: DF (0.23%), PB (10.74%), Ls (8.18%) and Gd (9.45%) (Fig. 3h). By contrast, the selection performed with *RW* assigned to *TA* index, showed high gains for PB (−6.29%) and low gains for PH (−0.57%) and DF (−0.17%) and no gains were found for GY (−1.08%) (Fig. 3i). Similar results were found when *RW* were used as economic weight to *SH* and *TA* indices (Fig. 3f and i). In other words, no gains were found for GY, Ls and Gd, indicating that the random weights values chosen for us, not provided a good linear combination to improve the CNA 12 population. This result can be noted by the means of selected progenies, mainly through the average of grain yield and diseases (leaf scald and grain discoloration) (Fig. 4a and e–f).

Discussion

Our field screening brought out systematic highly significant effects of progenies and environments, as well as frequent interaction effects, confirming the great performance of our field trials (Fig. 1). This can be noted by CVs values, despite high CVs, as commonly found when rice diseases are evaluated (Fig. 1d–f) (Cordeiro and Rangel 2011; Jackson et al. 2018). On the other hand, CV values showed to GY, PH and DF were lower than the values generally found in rice trials (Fig. 1a–c) (Costa et al. 2002; Morais Júnior et al. 2017b), allowing high accuracy in the estimates of target traits.

The range of the means found for the phenotypic data of CNA 12 population (Fig. 1a), were close to the values found by Soares et al. (2005) for grain yield and Cordeiro and Rangel (2011) for rice diseases (panicle blast, leaf scald and grain discoloration) (Fig. 1d–f). By contrast the averages found for PH and DF were lower than the values found for Cargnin et al. (2010) (Fig. 1b–c). Plant height reduction, is a desirable trait to be considered in rice breeding programs, once, rice cultivars with short stature are more resistant to lodging (Kashiwagi et al. 2008; Zhu et al. 2016). The reduction in plant height is associated with the introduction of *semidwarf 1* (*sd1*) gene, introduced from IR8 cultivar (Athwal 1971; Hargrove and Cabanilla 1979; Khan et al. 2015). Through this cultivar, it was possible to increase the levels of mineral fertilizers (e.g. nitrogen), and improve harvest index and grain yield (Khush 1999; Ookawa et al. 2010; Sowadan et al. 2018). Thus, these results showed that the CNA 12 population has sufficient variability and may be able to generate transgressive for the different evaluated traits, since the performance of the evaluated progenies was close to the performance of advanced breeding lines (controls).

It is well known that the G x E interaction and genotypic stability are large importance in rice breeding. Rice breeders prefer lines which are distinguished by high grain yield, good grain quality and are able to adapting to wide range of environments (Champagne et al. 2004; Dixit et al. 2015; Zhou et al. 2019). The existence of differentiated linear performance of the progenies for the evaluated environments (Fig. 1), was due to the influence of environmental factors, once these factors are highly dynamic and constantly changing during crop season (Li et al. 2018). These can be noted by the large estimates of R^2 for E, P(T) and ExP(T), suggesting that the agro-ecological conditions (temperature, luminosity, air humidity, soil fertility and disease pathogens) were diverse, and accounted for most variation in GY, DF, Ls and Gd (Fig. 2a, c and e–f). Thus, becomes important to understand the relationship between these genetic traits and the environments to improve the CNA 12 progenies.

In a breeding program, it is important the estimates of genetic parameters (albeit simplified). Through these estimates it is possible to identify the potential of segregating population, such as the population variability and the nature of the genes action involved in the control of quantitative traits. Moreover, through these parameters, it is possible to evaluate the efficiency of different breeding strategies, allowing

the maintenance of adequate genetic basis and more efficiency in the selection process (Almeida et al. 2014; Martins et al 2016; Alvares et al 2016; Silva et al. 2016b). Thus, the low variability displayed by DF and PH ($CV_g < 10\%$) (Fig. 2c and b) (Subramanian and Menon 1973) was not detrimental for selection of superior progenies, mainly for grain yield, once the average for the evaluated progenies were lower than control average (Fig. 1c and b), indicating greater probability to select superior progenies. Oppositely, PB, Ls and Gd had moderate ($10\% < CV_g < 20\%$) to high ($CV_g > 20\%$) CV_g values (Subramanian and Menon 1973), indicating greater genetic variability for these traits (Fig. 2d–f). Similar results were found by Aditya and Bhartiya (2013); Sangaré et al. (2017) and Tiwari et al. (2019). However, the estimate of CV_g alone is not much useful to determining the heritable portion of a trait (Jain et al. 2011). In this way, more reliability with selection can be achieved through association of this parameter with heritability estimates.

Heritability (h^2) is a useful parameter, because reflects the reliability in the phenotypes observed providing more accuracy in the selection of individuals genotypically superior (Ramalho et al. 2013). In previous studies, as conducted by Idris et al. (2012); Sumanth et al. (2017); Girma et al. (2018) and Alves et al. (2020) were found high estimates for broad-sense heritability for grain yield, leaf scald and panicle blast. These values, not corroborate with the results found here, once GY, PB and Ls showed moderate broad-sense heritability (30–60%) (Fig. 2a and d–e) (Johnson et al. 1955; Babu et al. 2012). This disagreement was not surprising, because broad-sense heritability is not only a trait property, but also, it is a population property, being sampled within each environment (Ramalho et al. 1993; Wray and Visscher 2008). It is known that grain yield is highly affected by environmental factors (Shrestha et al. 2012; Hossain et al. 2013; Ran et al. 2018). Moreover, there is high pathogenic variability for panicle blast (Zhu et al. 2000; Santos et al. 2017). In this way, the greater influence of environmental effects ($\sigma_e^2 > \sigma_g^2$) under phenotypic variation (σ_P^2) contributed to increase the deviation in phenotypic pattern, reducing h^2 estimates for these traits, and influencing directly the estimates for *b*-variation index for GY and PB, which were lower than 1.0 (Fig. 2a and d). This finding is similar to results found for grain yield in rice by Morais Júnior et al. (2017b) and wheat by Fellahi et al. (2018).

By contrast, broad-sense heritability was high ($h^2 > 60\%$) (Johnson et al. 1955; Babu et al. 2012), for PH, Gd and DF (Fig. 2b, f and c), indicating that, in the next generation these traits have greater probability of expression in the selected progenies and may be exploited by breeders. This finding was close to the results found by Sathya and Jebaraj (2013); Tuhina-Khatun et al. (2015); Alves et al. (2020). Coupled with this finding, *b*-variation index showed high values for the same traits. When *b*-variation values are equal or larger than 1.0, suggests greater genetic variability, indicating that the selection is highly favorable for the traits under evaluation (Vencovsky 1987; Mistro et al. 2004; Mendes et al. 2018).

The main factors which may interfere under the selection gains are the intensity of selection, the genetic properties of the population and the environmental conditions (Silva et al. 2020). Thus, the selection gains are directly related to the difference of means between selected groups and the original population. Here, the main reason for the lower gain displayed by *DS* for GY in relation to the gains found for DF, PB, Ls and Gd (Fig. 3a and c–d) can be due to conception of CNA 12 population. In the selection of S_1 plants, were considered only highly heritable traits (as plant height, days to flowering, grain shape, lodging resistance and resistance to diseases). Grain yield was prioritized only in the selection of $S_{1:3}$ progenies which, was carried out in multi-environment trials. On the other words, in the early stages of selection of CNA 12 population, grain yield was considered as secondary trait and the traits as grain quality, plant architecture and disease resistance, normally considered as secondary traits were prioritized (Morais Júnior et al. 2017a).

DS displayed higher gains in relation to other selection methods (Fig. 3a). However, through this method only one trait can be improved at a time. Likewise, favorable or unfavorable changes can will occur in the desirable traits. These responses will be dependent to the association level between the traits to be improved (Santos and Araújo 2001; Cruz and Carneiro 2006; Silva et al. 2008b). Thus, the multi-trait selection performed by selection indices can be more advantageous in relation to direct selection, once, is able to provide homogeneous gains in all the

traits, without meaningful losses in the main traits and can to overcome the limitation caused by the trait relationship (Costa et al. 2008; Lalić et al. 2010; Cruz 2012).

Our study showed that *MM* index provided the best gains in relation to *DS*, *IS*, *SH* and *TA* indices (Fig. 3). This index, maximized the gains in the CNA 12, once, the best behavior for the population average was found with him (Fig. 4). Crosbie et al. (1980) recorded *MM* index has some advantages under the others selection indices which need of weights assignment as *SH* index, such as: (*i*) is not affected by the inequality of variances between the measured traits, (*ii*) not require the estimation of genetic parameters, (*iii*) simplicity of use and, (*iv*) better selection differentials and predicted gains in each trait. An important aspect in the use of selection indices are the assignment of meaningful economic weights, and this is a main bottleneck for its use by breeders (Rodríguez et al. 1998; Bernardo 2002; Haskell et al. 2014). Here, *MM* index was used without the assignment of economic weights. Thus, the gains displayed by *MM* index were exclusively derived from the ranking of evaluated progenies, which facilitates its adoption in the routine of a breeding program due to its simplicity of estimation. Similar results were found in wheat (Fellahi et al. 2018; Meier et al. 2019), maize (Crevalari et al. 2017; Oloyede-Kamiyo 2019), sugarcane (Almeida et al. 2014; Azeredo et al. 2017) and soybean (Costa et al. 2004; Bizari et al. 2017).

Our results also showed that predicted gains displayed by *SH* and *TA* indices were very sensitive to economic weights assignment for each trait (Fig. 3d–i). The performance of *SH* index was especially poor when *RW* were assigned as economic weight. Similar results were found for *TA* index, when *b*-variation index and *RW* were assigned as economic weights (Fig. 3e–f and h–i), showing our difficulty to assign meaningful economic weights, hindering us to get simultaneous genetic gains for all the traits. This finding, can be linked with equal economic weights assigned to DF, PB, Ls and Gd. According to Crosbie et al. (1980) when is assigned equal economic weights for the different evaluated traits, most weight is placed on the trait with larger genetic variance, and less weight is given to the traits with lower genetic variance.

Conclusions

This study showed that CNA 12 population displayed wide phenotypic diversity, warranting further improvement for lowland rice. Thus, the CNA 12 population can be used in breeding program for development and exploitation of rice lines with greater grain yield and more stability for the main rice diseases. As waited *DS* provided high gains for all evaluated traits, however, we found it was possible to get considerable gains through selection indices. The results found here, showed clearly that between the different multi-trait selection criteria evaluated, *MM* index provided larger gains in relation to *SH* and *TA* indices. Furthermore, *MM* index is easy to implement in relation to other two indices, once, it is not necessary to assign economic weights to its procedure of estimation. Moreover, when the random weights were assigned to *SH* and *TA* indices, we did not find gains for the most measured traits, showing our difficult to assign meaningful economic weights to different traits under selection.

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Authors' contributions ACCC, PPT, PHNR and APC designed the experiments. ACCC, PPT, PHRG and APC phenotyped the panel. PHRG performed the statistical analysis. PHRG and PGSM interpreted the phenotypic results and wrote the paper, which was edited and approved by all co-authors.

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Availability of data and material All data generated or analysed during this study are included in this published article. The phenotypic data are included in Fig. 1.

Declarations

Conflicts of interest The authors declare that they have no competing interests.

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